

SEQUENCE LISTING

<110> MERCK-SANTE
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS)

<120> Insulin-induced gene as therapeutic target in diabetes

<130> BFF 03P0004

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 1062

<212> DNA

<213> Rattus sp.

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acagcccacc tggacctgtc ttccaaccgg ctagaaaccg	240
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acgcccactg ctttctcccg ctttcgtac ctggagtcac	360
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<210> 2

<211> 353

<212> PRT

<213> Rattus sp.

<400> 2

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20 25 30

Gly Leu Phe Asp Ser Phe Ser Leu Ile Arg Val Asp Cys Ser Ser Leu
35 40 45

Gly Pro His Ile Val Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu
50 55 60

Asp Leu Ser Ser Asn Arg Leu Glu Thr Val Asn Glu Ser Val Leu Gly
65 70 75 80

Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu
85 90 95

Leu Thr Ser Ile Thr Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu
100 105 110

Ser Leu Asp Leu Ser His Asn Gly Leu Ala Ala Leu Pro Ala Glu Val
115 120 125

Phe Thr Ser Ser Pro Leu Ser Asp Ile Asn Leu Ser His Asn Arg Leu
130 135 140

Arg Glu Val Ser Ile Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala
145 150 155 160

Leu His Val Asp Leu Ser His Asn Leu Ile His Arg Leu Leu Pro Tyr
165 170 175
Pro Ala Arg Ala Ser Leu Ser Ala Pro Thr Ile Gln Ser Leu Asn Leu
180 185 190

Ser Trp Asn Arg Leu Arg Ala Val Pro Asp Leu Arg Asp Leu Pro Leu
195 200 205

Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Thr Ile Asn Pro Gly
210 215 220

Ala Phe Met Gly Leu Ala Gly Leu Thr His Leu Ser Leu Ala Ser Leu
225 230 235 240

Gln Gly Ile Leu Gln Leu Pro Pro His Gly Phe Arg Glu Leu Pro Gly
245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Lys Trp Ala Gly
260 265 270

Ala Glu Val Phe Ser Gly Leu Gly Leu Leu Gln Glu Leu Asp Leu Ser
275 280 285

Gly Ser Ser Leu Val Pro Leu Pro Glu Thr Leu Leu His His Leu Pro
290 295 300

Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Gln Cys Arg Arg Leu
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Val Arg Glu Gly Ala Val His Arg Gln Pro Gly Ser Ser Pro Lys Val
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Val Leu His Cys Gly Asp Thr Gln Glu Ser Ala Arg Gly Pro Asp Ile
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<210> 3

<211> 2557

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1075)

<223>

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 Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
 255 260 265

tgg gca gga gct gag gtg ttt tca ggc ctg agc tcc ctg cag gag ctg 865
 Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
 270 275 280

gac ctt tcg ggc acc aac ctg gtg ccc ctg cct gag gcg ctg ctc ctc 913
 Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 285 290 295 300

cac ctc ccg gca ctg cag agc gtc agc gtg ggc cag gat gtg cgg tgc 961
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
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cg^g ccg ctg gtg cg^g gag gg^c acc tac ccc cg^g agg cct gg^c tcc agc 1009
 Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
 320 325 330

ccc aag gtg gcc ctg cac tgc gta gac acc cg^g gaa tct gct gcc agg 1057
 Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
 335 340 345

ggc ccc acc atc ttg tga c^aatgg^tgt ggcccagg^ggc cacataacag 1105
 Gly Pro Thr Ile Leu
 350

actgctgtcc tgggctgcct caggcccga gtaacttatg ttcaatgtgc caacaccagt 1165
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<210> 4

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (121)..(121)

<223> 'Xaa' in position 121 represents Ala or Thr.

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20 25 30

Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser Gly Leu Gly
35 40 45

Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu Asp
50 55 60

Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu Ser Val Leu Ala Gly
65 70 75 80

Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu Leu
85 90 95

Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu Ser
100 105 110

Leu Asp Leu Ser His Asn Gly Leu Xaa Ala Leu Pro Ala Glu Ser Phe
115 120 125

Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser His Asn Gln Leu Arg
130 135 140

Glu Val Ser Val Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala Leu
145 150 155 160

His Val Asp Leu Ser His Asn Ile His Arg Leu Val Pro His Pro
165 170 175

Thr Arg Ala Gly Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala
180 185 190

Trp Asn Arg Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg
195 200 205

Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala
210 215 220

Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
225 230 235 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly Leu
245 250 255

Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala Gly Ala
260 265 270

Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp Leu Ser Gly
275 280 285

Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu His Leu Pro Ala
290 295 300

Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys Arg Arg Leu Val
305 310 315 320

Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser Pro Lys Val Ala
325 330 335

Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg Gly Pro Thr Ile
340 345 350

Leu

<210> 5

<211> 25

<212> DNA

<213> Artificial : primer

<400> 5

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25

<210> 6

<211> 31

<212> DNA

<213> Artificial : primer

<400> 6

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31

<210> 7

<211> 22

<212> DNA

<213> Artificial : primer

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22

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<212> DNA

<213> Artificial : primer

<400> 8

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29

1